

FIG. I A

CCTGAAGGGAGAGCAGGGAGAGGACAGTGCGGCCAGAGGGCTCTGGGCACTGGAGG
 10
 GACGGCTCTTCTGCCAGGGGTCCCTGGGGATGGGATCACGCCAGAAGAAATGCCAG
 70
 AGAACGCAGCCTTTGAGAAGGGAAAGTCACTATCCCAGAGCCAGACTGAGCGGATGGAGTT
 130
 M E L
 190
 GAGGAAAGTACGGCCCTGGAAAGACTGGCGGGACAGTTATAGGAGGGCTTGCTCAGAGTAA
 R K Y G P G R L A G T V I G G A A Q S K
 250
 ATCACAGACTAAATCAGACTCAAATCACAAAGAGTTCCCTGCAGGCCCTTACACAGCCCC
 S Q T K S D S I T K E F L P G L Y T A P
 270
 TTCCCTCCCGTTCCCGCCCTCACAGGTGAGTGACCAAGTGCTAAATGACGCCAGGCT
 310
 S S P F P P S Q V S D H Q V L N D A E V
 370
 TGCCGCCCTCCCTGGAGAACTTCAGCTCTCAGCTATGAGACTATGGAGAAAACGAGAGTGACTC
 A A L L E N F S S S Y D Y G E N E S D S
 430
 GTGGCTGTACCTCCCGCCCTGGCCACAGGACATTCAAGCTTGAACTTGACCCGCTTCCT
 C C T S P P C P Q D F S L N F D R A F L
 490
 530

MATCH WITH FIG. I B

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FIG. I B
MATCH WITH FIG. IA

MATCH WITH FIG. 1B

F | G. | C

970	990	1010
GGTGCCTGCAGCTGGTGGCTGGCTTCTGCTGCCCTGCTGGTCATGGCCTACTGCTATGC		
V L Q L V A G F L L P L L V M A Y C Y A		
1030	1050	1070
CCACATCCCTGGCCCGTGCCTGGTTCCAGGGGCCAGGGGCCCATGGGGCATGGGGCT		
H I L A V L L V S R G Q R R L R A M R L		
1090	1110	1130
GCTGGTGGTGGTGTGGCTGGCCTTGGCCCTCTGCTGGACCCCCCTATCACCTGGTGGTGCT		
V V V V V A F A L C W T P Y H L V V L		
1150	1170	1190
GGTGGACATCCCTCATGGACCTGGCCCTTGGCCCAACTGTGGCCGAGAAAGCAGGGT		
V D I L M D L G A L A R N C G R E S R V		
1210	1230	1250
AGACGTTGGCCAAGTCGGTCACCTCAGGCCCTGGGCTACATGCOACTGCTGGCTCAACCCGCT		
D V A K S V T S G L G Y M H C C L N P L		
1270	1290	1310
GCTCTATGCCTTGTAGGGCTCAAGTTCGGGAGGGATGCTGGATGCTGCTCTTGGCCCT		
L Y A F V G V K F R E R M W M L L R L		

MATCH WITH FIG. IC

FIG. ID

1330	1350	1370
G C P N Q R G L	CAGGGCAGGCATCGTC	TCCGGGGATTCA
1390	Q R Q P S S R R	D S S
1410	1430	
CTGGTCTGAGACCTCAGAGGCCTCCTACTCGGGCTTGAGGGGGAAATCCGGGCTCCCC		
W S E T S E A S Y S G L *		
1450	1470	1490
TTTCGCCACAGTCTGACTTCCCCGCATTCCAGGCTCCTCCCTCTGCCGGCTCTGG		
1510	1530	1550
CTCTCCCCAATATCCTCCGCTCCGGGACTCACTGGCAGCCCCAGCACACCAGGTCTCCC		
1570	1590	1610
GGGAAGCCACCCTCCAGCTCTGAGGACTGCACCATTGCCTTAGCTGCCAAGGCC		
1630	1650	1670
CATCCTGCCGCCGAGGTGGCTGGCTGAGGCCACTGCCCTCTCATTGGAAACTAAA		
1690	1710	1730
ACTTCATCTCCCAAGTGGCATACAAGGGAGTACAAGGCATGGCGTAGAGGGTGCTGCCCATGA		
1750	1770	1790
AGCCACAGCCCAGGCCTCCAGCTCAGCAGTGACTGTGGCCATGGTCCCCAAGACCTCTAT		
1810	1830	1850
ATTTGGTCTTTATTTATGTCATAAAACTCCTGCTAAATAACAAGATCG		
1870		
TCAGGAAAAAA		

FIG. 2A

54	DHQVLNDAEVAALLENFSSSYDYGENESDCCCTSPPCPQDFSLNFDR AFL	103
•	•	•
•	•	•
•	•	•
2	ESDSFEDFWKGEDLNSNYSYSSTLPPFLDAAPCEPE...	SLEINKYFYV 46
•	•	•
•	•	•
•	•	•
104	PALNSLLFLGLLGNNGAVAAVLLSRRRTALSSTDTFLHLAWADTLLVL TLL	153
•	•	•
•	•	•
•	•	•
47	VIIYALVFLLSLGNMLVILYSGRSVTDVYLLNLAIDLFFALT L 96	•
•	•	•
•	•	•
•	•	•
154	PLWAVDAAVQWVFGSGLCKVAGALENNINFYAGALLACISFDRYLNIVHA	203
•	•	•
•	•	•
•	•	•
97	PIWAASKVNGWIFGTFLCKVVSILKEVNINFYSGILLACISVDRYLAIVHA	146
•	•	•
•	•	•
204	TQLYRRGPPARVTILTCLAVWGLCLLFALPDFIFLSAHHDERLNATHC QYN	253
•	•	•
•	•	•
147	TRTLTO.KRYLVKFICLISIWGLSLLALPVILLFRRTVYSSNVSPACYEDM	195
•	•	•
254	FPQVG..RTALRVLQLVAGFLLPPLLVMAYCYAHILAVLLVSRGQRRL RAM	301
•	•	•
•	•	•
196	CNNNTANWPMLIPVIPOSEGETIVYPI.L.TM.FCYGETI.RTLEKAHMGOKXH RAM	245
•	•	•

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MATCH WITH FIG. 2A

F | G . 2B

302	RLVVVVVVAFALCWTPTYHILVVDIILMDLGALLARNCGRESRVDVAKSVTS	351
246	RVIFAVVLIFLLCWLPYNLVLADTLMRTQVIQETCERRNHIDRALDATE	295
352	GLGYMHCCLNPLLYAFVGVKFRERMWMILLRLGCPNQRQGLQRQPSSSSRRD	401
296	ILGILHSCLNPLIYAFIGQKFRHGLLKILAIHGLISKDSDLPKDSRPSSFVG	345
402	SSWSETSEA	410
346	SSSGHTSTT	354